Daniel S Rokhsar

List of Publications by Year
in descending order

156 papers	55,448 citations	4120 87 h-index	8370 147 g-index
165 all docs	165 docs citations	165 times ranked	49567 citing authors

#	Article	IF	Citations
1	Phytozome: a comparative platform for green plant genomics. Nucleic Acids Research, 2012, 40, D1178-D1186.	6.5	4,204
2	The Sorghum bicolor genome and the diversification of grasses. Nature, 2009, 457, 551-556.	13.7	2,642
3	The Chlamydomonas Genome Reveals the Evolution of Key Animal and Plant Functions. Science, 2007, 318, 245-250.	6.0	2,354
4	Community structure and metabolism through reconstruction of microbial genomes from the environment. Nature, 2004, 428, 37-43.	13.7	2,045
5	The Genome of the Diatom Thalassiosira Pseudonana: Ecology, Evolution, and Metabolism. Science, 2004, 306, 79-86.	6.0	1,862
6	The Draft Genome of Ciona intestinalis: Insights into Chordate and Vertebrate Origins. Science, 2002, 298, 2157-2167.	6.0	1,539
7	The amphioxus genome and the evolution of the chordate karyotype. Nature, 2008, 453, 1064-1071.	13.7	1,496
8	The Phaeodactylum genome reveals the evolutionary history of diatom genomes. Nature, 2008, 456, 239-244.	13.7	1,458
9	Whole-Genome Shotgun Assembly and Analysis of the Genome of Fugu rubripes. Science, 2002, 297, 1301-1310.	6.0	1,432
10	Sea Anemone Genome Reveals Ancestral Eumetazoan Gene Repertoire and Genomic Organization. Science, 2007, 317, 86-94.	6.0	1,423
11	Repeated polyploidization of Gossypium genomes and the evolution of spinnable cotton fibres. Nature, 2012, 492, 423-427.	13.7	1,204
12	A reference genome for common bean and genome-wide analysis of dual domestications. Nature Genetics, 2014, 46, 707-713.	9.4	1,159
13	Genome sequencing and analysis of the biomass-degrading fungus Trichoderma reesei (syn. Hypocrea) Tj ETQq1 1 0.784314 rgBT /Ov	9.4	1,116
14	Phytophthora Genome Sequences Uncover Evolutionary Origins and Mechanisms of Pathogenesis. Science, 2006, 313, 1261-1266.	6.0	1,059
15	The high-quality draft genome of peach (Prunus persica) identifies unique patterns of genetic diversity, domestication and genome evolution. Nature Genetics, 2013, 45, 487-494.	9.4	1,031
16	The genome of the choanoflagellate Monosiga brevicollis and the origin of metazoans. Nature, 2008, 451, 783-788.	13.7	1,006
17	The Amphimedon queenslandica genome and the evolution of animal complexity. Nature, 2010, 466, 720-726.	13.7	917
18	Reference genome sequence of the model plant Setaria. Nature Biotechnology, 2012, 30, 555-561.	9.4	864

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19	Superconductivity and the Quantum Hard-Core Dimer Gas. Physical Review Letters, 1988, 61, 2376-2379.	2.9	849
20	Genome evolution in the allotetraploid frog Xenopus laevis. Nature, 2016, 538, 336-343.	13.7	849
21	Genome sequence of the lignocellulose degrading fungus Phanerochaete chrysosporium strain RP78. Nature Biotechnology, 2004, 22, 695-700.	9.4	805
22	The Trichoplax genome and the nature of placozoans. Nature, 2008, 454, 955-960.	13.7	801
23	Topology of the resonating valence-bond state: Solitons and high-Tcsuperconductivity. Physical Review B, 1987, 35, 8865-8868.	1.1	795
24	The Selaginella Genome Identifies Genetic Changes Associated with the Evolution of Vascular Plants. Science, 2011, 332, 960-963.	6.0	794
25	The genome sequence of Bifidobacterium longum subsp. infantis reveals adaptations for milk utilization within the infant microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18964-18969.	3.3	748
26	The dynamic genome of Hydra. Nature, 2010, 464, 592-596.	13.7	743
27	The genome of Eucalyptus grandis. Nature, 2014, 510, 356-362.	13.7	725
28	The Genome of the Western Clawed Frog Xenopus tropicalis. Science, 2010, 328, 633-636.	6.0	708
29	Chromosome-scale shotgun assembly using an in vitro method for long-range linkage. Genome Research, 2016, 26, 342-350.	2.4	679
30	Early origins and evolution of microRNAs and Piwi-interacting RNAs in animals. Nature, 2008, 455, 1193-1197.	13.7	630
31	Reverse Methanogenesis: Testing the Hypothesis with Environmental Genomics. Science, 2004, 305, 1457-1462.	6.0	624
32	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	3.3	582
33	Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. Nature Biotechnology, 2014, 32, 656-662.	9.4	572
34	Insights into bilaterian evolution from three spiralian genomes. Nature, 2013, 493, 526-531.	13.7	564
35	The tiny eukaryote Ostreococcus provides genomic insights into the paradox of plankton speciation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7705-7710.	3.3	563
36	Genomics of the origin and evolution of Citrus. Nature, 2018, 554, 311-316.	13.7	552

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37	Genomic Analysis of Organismal Complexity in the Multicellular Green Alga Volvox carteri. Science, 2010, 329, 223-226.	6.0	536
38	The octopus genome and the evolution of cephalopod neural and morphological novelties. Nature, 2015, 524, 220-224.	13.7	506
39	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. Genome Research, 2008, 18, 1100-1111.	2.4	456
40	Sequence and genetic map of Meloidogyne hapla : A compact nematode genome for plant parasitism. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14802-14807.	3.3	443
41	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	2.4	443
42	The Genome Portal of the Department of Energy Joint Genome Institute. Nucleic Acids Research, 2012, 40, D26-D32.	6.5	439
43	The Genome of Naegleria gruberi Illuminates Early Eukaryotic Versatility. Cell, 2010, 140, 631-642.	13.5	399
44	The Capsella rubella genome and the genomic consequences of rapid mating system evolution. Nature Genetics, 2013, 45, 831-835.	9.4	374
45	Sequencing wild and cultivated cassava and related species reveals extensive interspecific hybridization and genetic diversity. Nature Biotechnology, 2016, 34, 562-570.	9.4	340
46	The DNA sequence and biology of human chromosome 19. Nature, 2004, 428, 529-535.	13.7	298
47	Genomic analysis of immunity in a Urochordate and the emergence of the vertebrate immune system: â€œwaiting for Godotâ€. Immunogenetics, 2003, 55, 570-581.	1.2	278
48	Suboptimization of developmental enhancers. Science, 2015, 350, 325-328.	6.0	268
49	The Cassava Genome: Current Progress, Future Directions. Tropical Plant Biology, 2012, 5, 88-94.	1.0	265
50	Anchoring and ordering <scp>NGS</scp> contig assemblies by population sequencing (<scp>POPSEQ</scp>). Plant Journal, 2013, 76, 718-727.	2.8	264
51	Genesis and Expansion of Metazoan Transcription Factor Gene Classes. Molecular Biology and Evolution, 2008, 25, 980-996.	3.5	262
52	A whole-genome shotgun approach for assembling and anchoring the hexaploid bread wheat genome. Genome Biology, 2015, 16, 26.	3.8	256
53	Deeply conserved synteny resolves early events in vertebrate evolution. Nature Ecology and Evolution, 2020, 4, 820-830.	3.4	250
54	Parallel Evolution of Nacre Building Gene Sets in Molluscs. Molecular Biology and Evolution, 2010, 27, 591-608.	3.5	239

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55	Insights into the red algae and eukaryotic evolution from the genome of Porphyra umbilicalis (Bangiophyceae, Rhodophyta). Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E6361-E6370.	3.3	233
56	Rapid whole-genome mutational profiling using next-generation sequencing technologies. Genome Research, 2008, 18, 1638-1642.	2.4	225
57	Gutzwiller projection for bosons. Physical Review B, 1991, 44, 10328-10332.	1.1	221
58	Anatomy and development of the nervous system of Nematostella vectensis, an anthozoan cnidarian. Developmental Neurobiology, 2009, 69, 235-254.	1.5	220
59	Hemichordate genomes and deuterostome origins. Nature, 2015, 527, 459-465.	13.7	217
60	A New Spiralian Phylogeny Places the Enigmatic Arrow Worms among Gnathiferans. Current Biology, 2019, 29, 312-318.e3.	1.8	201
61	Meraculous: De Novo Genome Assembly with Short Paired-End Reads. PLoS ONE, 2011, 6, e23501.	1.1	191
62	Fine-scale variation in meiotic recombination in Mimulus inferred from population shotgun sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19478-19482.	3.3	190
63	Microcollinearity between autopolyploid sugarcane and diploid sorghum genomes. BMC Genomics, 2010, 11, 261.	1.2	175
64	The NK Homeobox Gene Cluster Predates the Origin of Hox Genes. Current Biology, 2007, 17, 706-710.	1.8	159
65	The sequence and analysis of duplication-rich human chromosome 16. Nature, 2004, 432, 988-994.	13.7	156
66	Dynamic Processes Shape Spatiotemporal Properties of Retinal Waves. Neuron, 1997, 19, 293-306.	3.8	154
67	Nuclear-localized tiny RNAs are associated with transcription initiation and splice sites in metazoans. Nature Structural and Molecular Biology, 2010, 17, 1030-1034.	3.6	146
68	Promoter elements associated with RNA Pol II stalling in the Drosophila embryo. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7762-7767.	3.3	145
69	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. Nature, 2021, 590, 438-444.	13.7	144
70	Syntax compensates for poor binding sites to encode tissue specificity of developmental enhancers. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6508-6513.	3.3	139
71	A genomewide survey of developmentally relevant genes in Ciona intestinalis. Development Genes and Evolution, 2003, 213, 235-244.	0.4	138
72	Chordate evolution and the three-phylum system. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20141729.	1.2	132

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73	A genomewide survey of developmentally relevant genes in Ciona intestinalis. Development Genes and Evolution, 2003, 213, 222-234.	0.4	130
74	A genomewide survey of developmentally relevant genes in Ciona intestinalis. Development Genes and Evolution, 2003, 213, 213-221.	0.4	129
75	Acoel genome reveals the regulatory landscape of whole-body regeneration. Science, 2019, 363, .	6.0	125
76	Evidence for a microRNA expansion in the bilaterian ancestor. Development Genes and Evolution, 2007, 217, 73-77.	0.4	124
77	Symbiotic organs shaped by distinct modes of genome evolution in cephalopods. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3030-3035.	3.3	123
78	The evolutionary origin of hedgehog proteins. Current Biology, 2007, 17, R836-R837.	1.8	121
79	The deuterostome context of chordate origins. Nature, 2015, 520, 456-465.	13.7	121
80	Retinal Waves Are Governed by Collective Network Properties. Journal of Neuroscience, 1999, 19, 3580-3593.	1.7	120
81	Genome Assembly Improvement and Mapping Convergently Evolved Skeletal Traits in Sticklebacks with Genotyping-by-Sequencing. G3: Genes, Genomes, Genetics, 2015, 5, 1463-1472.	0.8	112
82	Rudimentary quasicrystallography: The icosahedral and decagonal reciprocal lattices. Physical Review B, 1987, 35, 5487-5495.	1.1	105
83	The space groups of axial crystals and quasicrystals. Reviews of Modern Physics, 1991, 63, 699-733.	16.4	105
84	The DNA sequence and comparative analysis of human chromosome 5. Nature, 2004, 431, 268-274.	13.7	102
85	Accelerated gene evolution and subfunctionalization in the pseudotetraploid frog Xenopus laevis. BMC Biology, 2007, 5, 31.	1.7	102
86	The genomic landscape of molecular responses to natural drought stress in Panicum hallii. Nature Communications, 2018, 9, 5213.	5.8	101
87	Real-space renormalization study of disordered interacting bosons. Physical Review B, 1992, 46, 3002-3008.	1.1	96
88	Young inversion with multiple linked QTLs under selection in a hybrid zone. Nature Ecology and Evolution, 2017, 1, 119.	3.4	94
89	A framework genetic map for Miscanthus sinensis from RNAseq-based markers shows recent tetraploidy. BMC Genomics, 2012, 13, 142.	1.2	87
90	Domain shuffling and the evolution of vertebrates. Genome Research, 2009, 19, 1393-1403.	2.4	86

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91	Deeply conserved synteny and the evolution of metazoan chromosomes. Science Advances, 2022, 8, eabi5884.	4.7	81
92	Early evolution of the LIM homeobox gene family. BMC Biology, 2010, 8, 4.	1.7	77
93	Whole genome comparisons of Fragaria, Prunus and Malus reveal different modes of evolution between Rosaceous subfamilies. BMC Genomics, 2012, 13, 129.	1.2	77
94	Topology and nematic ordering. Physical Review Letters, 1993, 70, 1650-1653.	2.9	75
95	A physical map of the highly heterozygous Populus genome: integration with the genome sequence and genetic map and analysis of haplotype variation. Plant Journal, 2007, 50, 1063-1078.	2.8	70
96	Pairing in doped spin liquids: Anyon versusd-wave superconductivity. Physical Review Letters, 1993, 70, 493-496.	2.9	68
97	Gradual polyploid genome evolution revealed by pan-genomic analysis of Brachypodium hybridum and its diploid progenitors. Nature Communications, 2020, 11, 3670.	5.8	67
98	Genome biology of the paleotetraploid perennial biomass crop Miscanthus. Nature Communications, 2020, 11, 5442.	5.8	67
99	The genetics of divergence and reproductive isolation between ecotypes of Panicum hallii. New Phytologist, 2015, 205, 402-414.	3.5	65
100	Mechanical Unfolding of a Î²-Hairpin Using Molecular Dynamics. Biophysical Journal, 2000, 78, 584-589.	0.2	63
101	Conservation of linkage and evolution of developmental function within the Tbx2/3/4/5 subfamily of T-box genes: implications for the origin of vertebrate limbs. Development Genes and Evolution, 2008, 218, 613-628.	0.4	60
102	The Information Content of Spontaneous Retinal Waves. Journal of Neuroscience, 2001, 21, 961-973.	1.7	58
103	Parallel De Bruijn Graph Construction and Traversal for De Novo Genome Assembly. , 2014, , .		58
104	HipMer. , 2015, , .		57
105	A chromosomeâ€scale reference genome of trifoliate orange (Poncirus trifoliata) provides insights into disease resistance, cold tolerance and genome evolution in Citrus. Plant Journal, 2020, 104, 1215-1232.	2.8	56
106	Plant Pan-Genomics Comes of Age. Annual Review of Plant Biology, 2021, 72, 411-435.	8.6	56
107	Excited states of a dilute Bose-Einstein condensate in a harmonic trap. Physical Review A, 1998, 57, 1191-1201.	1.0	53
108	Quasicrystalline Textures of Cholesteric Liquid Crystals: Blue Phase III?. Physical Review Letters, 1986, 56, 1727-1730.	2.9	51

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109	QTL Mapping for Pest and Disease Resistance in Cassava and Coincidence of Some QTL with Introgression Regions Derived from Manihot glaziovii. Frontiers in Plant Science, 2017, 8, 1168.	1.7	51
110	A Genome-Wide Survey of Switchgrass Genome Structure and Organization. PLoS ONE, 2012, 7, e33892.	1.1	50
111	A New Nomenclature of Xenopus laevis Chromosomes Based on the Phylogenetic Relationship to Silurana/Xenopus tropicalis. Cytogenetic and Genome Research, 2015, 145, 187-191.	0.6	50
112	Topology and nematic ordering. I. A gauge theory. Physical Review E, 1995, 52, 1778-1800.	0.8	48
113	Scale equivalence of quasicrystallographic space groups. Physical Review B, 1988, 37, 8145-8149.	1.1	47
114	Genome and transcriptome mechanisms driving cephalopod evolution. Nature Communications, 2022, 13, 2427.	5.8	47
115	Chromosomal mapping of 170 BAC clones in the ascidian Ciona intestinalis. Genome Research, 2005, 16, 297-303.	2.4	45
116	Quadratic quantum antiferromagnets in the fermionic large-Nlimit. Physical Review B, 1990, 42, 2526-2531.	1.1	44
117	Identical Genomic Organization of Two Hemichordate Hox Clusters. Current Biology, 2012, 22, 2053-2058.	1.8	43
118	A chromosome-scale genome assembly and dense genetic map for Xenopus tropicalis. Developmental Biology, 2019, 452, 8-20.	0.9	43
119	Beware of 46-Fold Symmetry: The Classification of Two-Dimensional Quasicrystallographic Lattices. Physical Review Letters, 1987, 58, 2099-2101.	2.9	42
120	Disordered bosons: Condensate and excitations. Physical Review B, 1994, 49, 9013-9023.	1.1	40
121	QTL associated with resistance to cassava brown streak and cassava mosaic diseases in a bi-parental cross of two Tanzanian farmer varieties, Namikonga and Albert. Theoretical and Applied Genetics, 2017, 130, 2069-2090.	1.8	39
122	The Early ANTP Gene Repertoire: Insights from the Placozoan Genome. PLoS ONE, 2008, 3, e2457.	1.1	38
123	Chromosome evolution and the genetic basis of agronomically important traits in greater yam. Nature Communications, 2022, 13, 2001.	5.8	35
124	Terabase-scale metagenome coassembly with MetaHipMer. Scientific Reports, 2020, 10, 10689.	1.6	34
125	Analysis of muntjac deer genome and chromatin architecture reveals rapid karyotype evolution. Communications Biology, 2020, 3, 480.	2.0	31
126	Diversification of mandarin citrus by hybrid speciation and apomixis. Nature Communications, 2021, 12, 4377.	5.8	31

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127	Ancient polymorphisms contribute to genome-wide variation by long-term balancing selection and divergent sorting in Boechera stricta. Genome Biology, 2019, 20, 126.	3.8	30
128	merAligner: A Fully Parallel Sequence Aligner. , 2015, , .		28
129	A detailed gene expression study of the Miscanthusgenus reveals changes in the transcriptome associated with the rejuvenation of spring rhizomes. BMC Genomics, 2013, 14, 864.	1.2	27
130	Development of a toolbox to dissect host-endosymbiont interactions and protein trafficking in the trypanosomatid Angomonas deanei. BMC Evolutionary Biology, 2016, 16, 247.	3.2	26
131	The Eucalyptus grandisGenome Project: Genome and transcriptome resources for comparative analysis of woody plant biology. BMC Proceedings, 2011, 5, .	1.8	25
132	Assembly of the Boechera retrofracta Genome and Evolutionary Analysis of Apomixis-Associated Genes. Genes, 2018, 9, 185.	1.0	24
133	Phylogenomics illuminates the evolution of bobtail and bottletail squid (order Sepiolida). Communications Biology, 2021, 4, 819.	2.0	24
134	Analysis of meiosis in Pristionchus pacificus reveals plasticity in homolog pairing and synapsis in the nematode lineage. ELife, 2021, 10, .	2.8	21
135	Electronic pairing mechanism in fullerenes: Interactions and correlations. Physical Review B, 1993, 48, 4103-4113.	1.1	20
136	Populus resequencing: towards genome-wide association studies. BMC Proceedings, 2011, 5, .	1.8	19
137	A proposal to sequence the amphioxus genome submitted to the joint genome institute of the US department of energy. The Journal of Experimental Zoology, 2003, 300B, 5-22.	1.4	17
138	The origin of citrus. , 2020, , 9-31.		15
139	Rosaceaous Genome Sequencing: Perspectives and Progress. , 2009, , 601-615.		14
140	Old can be new again: HAPPY whole genome sequencing, mapping and assembly. International Journal of Biological Sciences, 2009, 5, 298-303.	2.6	14
141	Stacking quasicrystallographic lattices. Physical Review B, 1990, 41, 10498-10502.	1.1	12
142	Topology and nematic ordering. II. Observable critical behavior. Physical Review E, 1995, 52, 1801-1810.	0.8	12
143	A segmental genomic duplication generates a functional intron. Nature Communications, 2011, 2, 454.	5.8	12
144	Current status and impending progress for cassava structural genomics. Plant Molecular Biology, 2022, 109, 177-191.	2.0	11

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145	Isotopic disorder in superconducting fullerenes. Physical Review B, 1993, 48, 4114-4118.	1.1	10
146	New bobtail squid (Sepiolidae: Sepiolinae) from the Ryukyu islands revealed by molecular and morphological analysis. Communications Biology, 2019, 2, 465.	2.0	9
147	The citrus genome. , 2020, , 1-8.		7
148	Efficient and accurate clustering for large-scale genetic mapping. , 2014, , .		5
149	Development and Initial Characterization of A HAPPY Panel for Mapping the X. Tropicalis Genome. International Journal of Biological Sciences, 2011, 7, 1037-1044.	2.6	4
150	Genome organization of the vg1 and nodal3 gene clusters in the allotetraploid frog Xenopus laevis. Developmental Biology, 2017, 426, 236-244.	0.9	4
151	Beyond â€œliving fossilsâ€• Can comparative genomics finally reveal novelty?. Molecular Ecology Resources, 2022, 22, 9-11.	2.2	2
152	Constrained spin model of phason dynamics in quasicrystals. Physical Review B, 1990, 42, 8517-8536.	1.1	1
153	Condensates in a twist. Nature, 1999, 401, 533-534.	13.7	0
154	COMPARATIVE PAIR-WISE DOMAIN-COMBINATIONS FOR SCREENING THE CLADE SPECIFIC DOMAIN-ARCHITECTURES IN METAZOAN GENOMES. , 2007, , .		0
155	A Two-Layer Model Describes the Spatiotemporal Properties of Spontaneous Retinal Waves. , 1998, , 337-342.		0
156	Sequence and Assembly of the Soybean Genome. , 2008, , 101-112.		0